Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

1–47. (canceled)

48. (new) A method of detecting one or more target sequences in a sample, the method comprising the steps of:

forming one or more closed circular probes whenever a first targeting domain and a second targeting domain of any of a plurality of precircle probes hybridize with their respective first target domains and second target domains of the one or more target sequences such that 5' and 3' nucleotides of the respective precircle probes abut one another, each precircle probe further having at least a first universal primer site and a cleavage site;

cleaving the one or more closed circular probes to form cleaved probes;

amplifying cleaved probes using a first universal primer complementary with a first universal primer site to form one or more amplicons; and

detecting the amplicons to detect the one or more target sequences in the sample.

49. (new) The method of claim 48 further comprising the step of digesting said precircle probes prior to said step of cleaving said closed circular probes.

50. (new) The method of claim 49 wherein each of said precircle probes further includes a barcode sequence that is unique to said precircle probe.

51. (new) The method of claim 50 wherein each of said one or more amplicons comprises said barcode sequence and is detected by said barcode sequence.

52. (new) The method of claim 51 wherein said step of detecting includes hybridizing said barcode sequences to a probe array.

53. (new) The method of 52 wherein each of said precircle probes further has a second universal primer site such that said cleavage site is between said first universal primer site and the second universal primer site.

54. (new) The method of claim 53 wherein said one or more amplicons are made in a polymerase chain reaction using said first universal primer and a second universal primer complementary to said second universal primer site.

55. (new) The method of claim 54 wherein said step of digesting includes treating said sample with an exonuclease and denaturing the exonuclease prior to said step of cleaving.

56. (new) The method of claim 54 wherein said step of detecting said amplicons includes hybridizing a label probe to a portion of each of said amplicons.

57. (new) The method of claim 56 wherein said label probe has a primary label that is directly detected.

58. (new) The method of claim 56 wherein said label probe has a secondary label comprising a hapten.

59. (new) The method of claim 56 wherein said label probe has a secondary label comprising biotin.

60. (new) The method of claim 52 wherein said one or more target sequences each have a gap domain between said first target domain and said second target domain and wherein said step of forming said closed circular probe includes the steps of extending said first targeting domain along the gap domain by a polymerase so that it is abutting said second targeting domain; and ligating said first targeting domain to said second targeting domain, thereby forming said closed circular probe.

61. (new) The method of 60 wherein each of said precircle probes further has a second universal primer site such that said cleavage site is between said first universal primer site and the second universal primer site.

62. (new) The method of claim 61 wherein said one or more amplicons are made in a polymerase chain reaction using said first universal primer and a second universal primer complementary to said second universal primer site.

63. (new) The method of claim 62 wherein said step of digesting includes treating said sample with an exonuclease and denaturing the exonuclease prior to said step of cleaving.

64. (new) The method of claim 52 wherein said one or more target sequences each have a gap domain between said first target domain and said second target domain and wherein said step of forming said closed circular probe includes the step of ligating a gap oligonucleotide complementary to the gap domain to said first targeting domain and said second targeting domain, thereby forming said closed circular probe.

65. (new) The method of claim 64 wherein said step of ligating includes treating said sample with a ligase.

66. (new) The method of claim 65 wherein said gap domain is between 1 and 500 nucleotides.

67. (new) The method of claim 52 wherein said said first targeting domain abuts said second targeting domain and wherein said step of forming said closed circular probe includes

ligating said first targeting domain to said second targeting domain, thereby forming said closed circular probe.

68. (new) The method of claim 67 wherein said step of ligating includes treating said sample with a ligase.

69. (new) A method of amplifying one or more target sequences, the method comprising the steps of:

forming one or more closed circular probes whenever a first targeting domain and a second targeting domain of any of a plurality of precircle probes hybridize with their respective first target domains and second target domains of the one or more target sequences such that 5' and 3' nucleotides of the respective precircle probes abut one another, each precircle probe further having at least a first universal primer site and a cleavage site;

cleaving the one or more closed circular probes to form cleaved probes;

amplifying cleaved probes using a first universal primer complementary with a first universal primer site to form one or more amplicons.

70. (new) The method of 69 wherein each of said precircle probes further has a second universal primer site such that said cleavage site is between said first universal primer site and the second universal primer site.

71. (new) The method of claim 70 wherein said one or more amplicons are made in a polymerase chain reaction using said first universal primer and a second universal primer complementary to said second universal primer site.